Attachment to Paper 6

FORM PTO-1449 (Modified)

LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT

ATTY. DOCKET NO. 24737-1906B	SERIAL NO. 09/704,362
APPLICANT Ramnarayan *et al.*	
FILING DATE November 1, 2000	GROUP ~~2857~~ 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
JB		0 1 3 5 3 1 6	05/17/01	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

EXAMINER J.S. Bruce | DATE CONSIDERED 8/8/02

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attachment to Paper 8

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906B	SERIAL NO. 09/704,362
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	RECEIVED
	FILING DATE November 01, 2000	GROUP ~~2857~~ 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
BS	AA	5,303,157	07/19/94	Balaji *et al.*	364	500	12/14/90
	AB	5,579,211	11/26/96	Balaji *et al.*	364	496	04/24/95
	AC	5,621,895	03/18/97	Balaji *et al.*	364	496	04/21/95
	AD	5,802,496	09/15/98	Arnaud *et al.*	367	103	12/04/95
	AE	5,837,464	11/17/98	Capon *et al.*	435	6	01/29/97
	AF	5,846,746	12/08/98	Lee *et al.*	435	69.1	05/13/94
	AG	5,910,408	06/08/99	Hlavka *et al.*	514	9	09/20/96

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
BS	AH	Duplicate	09/28/00	PCT				
BS	AI	9506293	03/02/95	PCT				
BS	AJ	9514028	05/26/95	PCT				
BS	AK	Duplicate	07/31/97	PCT				
BS	AL	Duplicate	07/31/97	PCT				
BS	AM	9806048	02/12/98	PCT				
BS	AN	9813781	04/02/98	PCT				
BS	AO	9854665	12/03/98	PCT				
BS	AP	Duplicate	02/11/99	PCT				

EXAMINER JB. Bunsa | DATE CONSIDERED 8/8/02

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Title: **USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS**

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906B	SERIAL NO. 09/704,362
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BB	AQ	Abagyan *et al.* "Biased Probability Monte Carlo Conformational Searches and Electrostatic Calculations for Peptides and Proteins," *J. Mol. Biol.* 235: 983-1002 (1994). Duplicated
BB	AR	Abdel-Meguid, S.S. *et al.* "An orally bioavailable HIV-1 protease inhibitor containing an imidazole-derived peptide bond replacement: crystallographic and pharmacokinetic analysis," *Biochemistry* 33(39):11671-11677 (1994)
BB	AS	Altschul *et al.* "Basic Local Alignment Search Tool," *J. Mol. Biol.* 215: 403-10 (1990). Duplicated
BB	AT	Balasubramanian, R. "New type of representation for mapping chain-folding in protein molecules," *Nature* 266: 856-57 (1977). Duplicated
BB	AU	Blaney, R. "Molecular modelling in the pharmaceutical industry, *Chemistry and Industry. Chemistry and Industry Review* 23(4):791-4 (1990).
not considered	AV	~~*Biocomputing: Informatics and Genome Projects* Smith, D.W., ed. Academic Press, Inc.,~~ San Diego (1994). no copy provided
BB	AW	Bohm,G. "New approaches in molecular structure prediction" *Biophysical Chemsitry* 59:1-32 (1996)
BB	AX	Bouras *et al.* "Design, Synthesis, and Evaluation of Conformationally Constrained Tongs, New Inhibitors of HIV-1 Protease Dimerization," *J. med. Chem* 42: 957-62 (1999). Duplicated
BB	AY	Carrillo, H. and D. Lipman., "The Multiple Sequence Alignment Problem in Biology," *SIAM J. Appl. Math.* 48(5): 1073-82 (1988). Duplicated
not considered	AZ	~~*Computational Molecular Biology: Sources and Methods for Sequence Analysis* Lesk,~~ A.M., ed. Oxford University Press, New York (1988) no copy provided
BB	BA	Devereux *et al.* "A comprhensive set of sequence analysis programs for the VAX," *nucl. Acids Res.* 12(1): 387-95 (1984). Duplicated
not considered	BB	Dialog #03523908 JICST Acc. No.: 98A0122627 English language description of Habuka, Noriyaki, "Crystal structure of HCV NS3 protease," *Jikken Igaku* 15(19): 2308-13 (1997). no translation or statement of relevance
BB	BC	Dudek *et al.* "Protein Structure Prediction Using a Combination of Sequence Homology and Global Energy Minimization: II. Energy Functions," *Journal Computational Chemistry* 19: 548-73 (1998). Duplicated
BB	BD	Goodsell, D.S. and A. J. Olson, "Automated Docking of Substrates to Proteins by Simulated Annealing," *Proteins: Structure Function, and Genetics* 8: 195-202 (1990). Duplicated

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JBB	BE	Gribskov, M. and R.R. Burgess., "Sigma factors from *E. coli, B. subtilis,* phage SP01, and phage T4 are homologous proteins," *Nucl. Acids Res.* 14(1): 6745-63 (1986). Duplicate
not considered	BF	~~*Guide to Human Genome Computing* Bishop, M., ed. Academic Press, Inc., San Diego (1994).~~ no copy provided
JBB	BG	Gulnik *et al.* "Kinetic Characterization and Cross-Resistance Patterns of HIV-1 Protease Mutants Selected under Drug Pressure," *Biochemistry* 35: 9282-7 (1995). Duplicate
not considered	BH	~~Habuka *et al.* "Crystal Structure of HCV NS3 protease," *Jikken Igaku* 15(19): 2308-13~~ (1997). no translation or statement of relevance
JBB	BI	Jacobsen *et al.* "Characterization of Human Immunoeficiency Virus Type 1 Mutanta with Decreased Sensitivity to Protease Inhibitor Ro 31-8959," *Virology* 206: 527-34 (1995). Duplicate
JBB	BJ	Kim *et al.* "Crystal Structure of the Hepatitis C virus Ns3 Protease Domain complexed with a Synthetic NS4A Cofactor Peptide," *Cell* 87: 343-355 (1996).
JBB	BK	Klabe *et al.* "Resistance to HIV Protease Inhibitors: a Comparison of Enzyme Inhibition and Antiviral Potency," *Biochemistry* 37: 8735-42 (1998).
JBB	BL	Kohlstaedt *et al.* "Crystal Structre at 3.5 Angstrom Resolution of HIV-1 Reverse Transcriptase Complexed with an Inhibitor," *Science* 256: 1783-1790 (1992).
	BM	Kroeger *et al.* "Molecular modeling of HIV-1 reverse transcriptase drug-resistant mutant strains; implications for the mechanism of polymerase action," *Protein Engineering* 10(12): 1379-1383 (1997).
	BN	Kuntz *et al.* "Structure-Based Strategies for Drug Design and Discovery," *Science* 257: 1078-82 (1992).
	BO	Kuntz *et al.* "A Geometric Approach to Macromolecule-Ligand Interactions," *J. Mol. Biol.* 161: 269-288 (1982).
	BP	Lambert, M., "Docking Conformationally Flexible Molecules into Protein Binding Sites," in *Practical Application of Computer-Aided Drug Design,* Charifson, ed. Mercel Dekker, NY, pp.243-303. (1997).
	BQ	Maschera *et al.* "Human Immunodeficiency Virus," *J. Biol. Chem.* 271(52): 33231-5 (1996). N/
not considered	BR	~~*Methods in Molecular Biology vol. 24; Computer Analysis of Sequence Data, Part 1:* Griffin, A. and H.G. Griffin, eds. Humana Press, Inc. Totowa, New Jersey (1994).~~ no copy provided

EXAMINER John S. Brusca | DATE CONSIDERED 8/8/02

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JBB	BD	Momany *et al.* "Energy Parameters in Polypeptides. VII. Geometric Parameters, Partial Atomic Charges, Nonbonded Interactions, Hydrogen Bond Interactions, and Intrinsic Torsional Potentials for the Naturally Occuring Amino Acids," *The Journal of Physical Chemistry* 79(22): 2361-81 (1975).
JBB	BT	Murcko, M.A., "An Introduction to De Novo Ligand Design," in *Practical Application of Computer-Aided Drug Design,* Charifson, ed. Mercel Dekker, NY, pp.305-354. (1997).
	BU	Needleman, S.B. and C.D. Wunsch., "A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins," *J. Mol. Biol.* 48: 443-53 (1970).
	BV	Nemethy *et al.* "Energy Parameters in Polypeptides. 10. Improved Geometrical Parameters and Nonbonded Interactions for Use in the EEPP/3 Algorithm, with Application to Proline-Containing Peptides," *J. Phys. Chem.* 96: 6472-84 (1992).
	BW	Pazhanisamy *et al.* "Kinetic Characterization of Human Immunodeficiency Virus Type-1 Protease-resistant Variants," *J. Biol. Chem.* 271(30): 17979-85 (1996).
	BX	Pearson, W.R. and D.J. Lipman., "Improved tools for biological comparison," *Proc. Natl. Acad. Sci. USA* 85: 2444-8 (1988).
JBB	BY	*QSAR and Drug Design: New Developments and Applications* T. Fugita, ed. Elsevier Science B.V. (1995) pp.3-81.
JBB	BZ	Ramnarayan *et al.* "The effect of polarization energy on the free energy perturbation calculation," *J. Chem. Phys.* 92(12): 7057-67 (1990).
not considered	CA	~~Richter, R., "AIDS drugs found to be effective in world's most common HIV strains" January 20, 1999.~~ no place of publication
JBB	CB	Schapira *et al.* "Prediction of the binding energy for small molecules, peptides, and proteins," *J. Mol. Recognition* 12: 177-90 (1999).
JBB	CC	Schwartz, R.M. and M.O. Dayhoff.," Matrices for Detecting Distant Relationships," Chapter 23 of: Atlas of Protein Sequence and Structure Dayhoff, M.O. ed. National Biomedical Research Foundation pp.353-8 (1978).
not considered	CD	~~*Sequence Analysis in Molecular Biology: Treasure Trove or Trivial Pursuit*~~ von Heijne, G., ed. Academic Press, Inc. San Diego (1987). copy not provided
JBB	CE	Shafer *et al.* "Human Immunodeficiency Virus reverse Transcriptase and Protease Sequence Database," *Nucl. Acids Res.* 27(1): 348-52 (1999).

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JSB	CF	Shafer *et al.* "Identification of Biased Amino Acid Substitution Patterns in Human Immunodeficiency Virus Type 1 Isolates from Patients Treated with Protease Inhibitors," *Journal of Virology* 73(7): 6197-6202 (1999).
JSB	CG	Shenderovich, *et al.*, "Structural Pharmacogenic Approach to the Evaluation of Drug Resistant Mutations and HIV-1 Protease", *Journal of Clinical Ligand Assay*, 24(2):140-144 (2001)
JSB	CH	Shoichet, B.K. and I.D. Kuntz, "Protein docking and Complementarity," *J. Mol. Biol.* 221: 327-46 (1991).
JSB	CI	Shoichet *et al.* "Structure-Based Discovery of Inhibitors of Thymidylate Synthase," *Science* 259: 1445-50 (1993).
JSB	CJ	Smith, T. F. and M. S. Waterman., "Comparison of Biosequences," *Adv. Appl. Math.* 2: 482-489 (1981).
JSB	CK	Stewart *et al.* "Automated 3D Decking: Inhibitors of α-Chymotrypsin," *Medicinal Chemistry Research* 1: 439-443 (1992).
JSB	CL	Thompson, S.K. *et al.* "Rational design, synthesis, and crystallographic analysis of a hydroxyethylene-based HIV-1 protease inhibitor containing a heterocyclic P1'-P2' amide bond isoster," *Journal of Medicinal Chemistry* 37(19):3100-3107 (1994).
JSB	CM	Wang and Kollman, "Computational study of protein specificity: The molecular basis of HIV-1 protease drug resistance", *PNAS*, 98(26):14937-14942 (2001).
JSB	CN	Weiner *et al.* "An All Atom Force Field for Simulations of Proteins and Nucleic Acids," *Journal of Computational Chemistry* 7(2): 230-52 (1986).

EXAMINER J.S. Brucea | DATE CONSIDERED 8/8/02

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Attachment to Paper 13

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906B	SERIAL NO. 09/704,362
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 1, 2000	GROUP ~~2857~~ 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
JB		4	2	0	8	4	7	9	06/17/80	Zuk *et al.*	~~435~~	~~7~~	07/14/77
		4	2	2	0	4	5	0	09/02/80	Maggio	~~23~~	~~230~~	04/05/78
		4	2	3	3	4	0	1	11/11/80	Yoshida *et al.*	~~435~~	~~7~~	07/14/77
		4	2	3	3	4	0	2	11/11/80	Maggio *et al.*	~~435~~	~~7~~	04/05/78
		4	2	7	7	4	3	7	07/01/81	Maggio	~~422~~	61	12/10/79
		4	3	8	5	1	2	6	05/24/83	Chen *et al.*	~~436~~	~~518~~	03/19/79
		4	3	9	7	9	5	6	08/09/83	Maggio	~~436~~	~~34~~	12/10/81
		4	7	8	6	4	7	1	11/22/88	Jones *et al.*	~~422~~	~~81~~	10/21/83
		4	7	8	9	6	3	1	12/06/88	Maggio	~~435~~	~~7~~	02/17/84
		4	8	2	8	9	8	1	05/09/89	Maggio	~~435~~	~~7~~	08/24/83
		4	8	5	9	6	1	0	08/22/89	Maggio	~~436~~	~~518~~	09/12/86
		5	0	7	9	1	4	2	01/07/92	Coleman *et al.*	~~435~~	~~92~~	01/23/87
		5	2	1	5	8	9	9	06/01/93	Dattagupta	~~435~~	~~6~~	08/23/90
		5	3	3	1	5	7	3	07/19/94	Balaji *et al.*	~~364~~	~~500~~	12/14/90
		5	5	7	1	8	2	1	11/05/96	Chan *et al.*	~~514~~	~~312~~	05/20/94
		5	5	7	9	2	5	0	11/26/96	Balaji *et al.*	~~364~~	~~496~~	04/24/95
		5	6	1	2	8	9	5	03/18/97	Balaji *et al.*	~~364~~	~~496~~	04/21/95
*		5	7	1	2	1	4	5	01/27/98	Houghton *et al.*	~~435~~	~~219~~	09/06/96
		5	8	0	8	9	6	9	09/15/98	Arnaud *et al.*	~~367~~	~~103~~	12/04/95
		5	8	3	7	4	6	4	11/17/98	Capon *et al.*	~~435~~	~~6~~	01/29/97
		5	8	4	6	7	6	3	12/08/98	Lee *et al.*	~~435~~	~~69.1~~	05/13/94
		5	9	1	0	4	7	8	06/08/99	Hlavka *et al.*	~~514~~	~~9~~	09/20/96

FOREIGN PATENT DOCUMENTS

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		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
JBS		00573097	09/28/00	PCT				
JBS		97273197	07/31/97	PCT				
JBS		97274804	07/31/97	PCT				
JBS		99065977	02/11/99	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

not considered	~~3D QSAR in Drug Design~~ Kubinyi, H (ed.) Kluwer Academic Publishers (1993). no copy provided	
JBS	✓	Abagyan *et al.* Biased Probability Monte Carlo Conformational Searches and Electrostatic Calculations for Peptides and Proteins, *J. Mol. Biol.* 235: 983-1002 (1994).
	✓	Abagyan *et al.* Protein structure prediction by global energy optimization, *Comput. Simul. Biomol. Syst.* 3:363-94 (1997).
*		Ajay *et al.*, Computational Methods to Predict Binding Free Energy in Ligand-Receptor Complexes, Journal of Medicinal Chemistry. 38(26):4953-4967 (1995).
	✓	Altschul, Gap costs for multiple sequence alignment, J. Theor. Biol., 138:297-309 (1989)
	✓	Altschul and Lipman, Trees, stars and multiple biological sequence alignment, SIAM J. Appl. Math., 49:197-209 (1989)
	✓	Altschul, Leaf pairs and tree dissections, SIAM J. Discrete Math., 2:293-299 (1989)
	✓	Altschul *et al.*, Weights for data related by a tree, J. Molec. Biol., 207:647-653 (1989)
	✓	Altschul *et al.* Basic Local Alignment Search Tool, *J. Mol. Biol.* 215: 403-10 (1990).
*		Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclopropane 1-carboxylic acid residues, Pept. Res. 7(2):60-71 (1994).
*		Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclobutane 1-carboxylic acid residues, Pept. Res. 8(3):178-86 (1995).
*		Balasubramaniam *et al.*, [D-TRP^{32}]Neuropeptide Y: A Competitive Antagonist of NPY in Rat Hypothalamus, J. Med. Chem. 37(6):811-815 (1994).
	✓	Balasubramanian, R., New type of representation for mapping chain-folding in protein molecules, *Nature* 266: 856-57 (1977).
	✓	Bernstein *et al.*, The protein data bank: a computer-based archival file for macromolecule structures, J. Mol. Biol., 112:535-542 (1977)

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not considered	✓	~~*Biocomputing: Informatics and Genome Projects*~~ Smith, D.W., ed. Academic Press, Inc., San Diego (1994). no copy provided
* JSB		Böhm, Prediction of binding constants of protein ligands: A fast method for the prioritization of hits obtained from de novo design or 3D database search programs, Journal of Computer-Aided Molecular Design. 12:309-323 (1998).
	✓	Bouras *et al.* Design, Synthesis, and Evaluation of Conformationally Constrained Tongs, New Inhibitors of HIV-1 Protease Dimerization, J. Med. Chem. *42:* 957-62 (1999).
	✓	Carrillo, H. and D. Lipman., The Multiple Sequence Alignment Problem in Biology, *SIAM J. Appl. Math.* 48(5): 1073-82 (1988).
	✓	Carson and Bugg, Algorithm for ribbon models of proteins, J. Mol. Graphics, 4:121-122 (1986)
	✓	Carson, Ribbons 2.0, J. Appl. Cryst., 24:958-961 (1991)
	✓	Carson, Ribbon models of macromolecules, J. Mol. Graphics, 5:103-106 (1987)
	✓	Carson, Ribbons, Methods in Enzymology, R.M. Sweet and C.W. Carter, eds, Academic Press, 277:493-505 (1997)
*		Checa *et al.*, Assessment of Solvation Effects on Calculated Binding Affinity Differences: Trypsin Inhibition by Flavonoids as a Model System for Congeneric Series, J. Med. Chem. 40:4136-4145 (1997).
not considered	✓	~~*Computational Molecular Biology: Sources and Methods for Sequence Analysis*~~ Lesk, A.M., ed. Oxford University Press, New York (1988) no copy provided
* JSB		Daniels, Blood group polymorphisms: molecular approach and biological significance, Transfus. Clin. Biol. 4:383-390 (1997).
*		Das *et al.*, Crystal Structures of 8-Cl and 9-Cl Complexed with Wild-type HIV-1 RT and 8-Cl TIBO Complexed with the Tyr181Cys HIV-1 RT Drug-resistant Mutant, J. Mol. Biol. 264:1085-1100 (1996).
	✓	Devereux *et al.* A comprhensive set of sequence analysis programs for the VAX, *nucl. Acids Res.* 12(1): 387-95 (1984).
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*		Eldridge *et al.*, Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of ligands in receptor complexes, Journal of Computer-Aided Molecular Design. 11:425-445 (1997).
*		Erickson *et al.*, Structural Mechanisms of HIV Drug Resistance, Annu. Rev. Pharmacol. Toxicol. 36:545-71 (1996).
*		Fox, S. Pharmacogenomics Thrives in Europe. Genetic Engineering News. June 15, 1999.
	✓	Goodsell, D.S. and A. J. Olson, Automated Docking of Substrates to Proteins by Simulated Annealing, *Proteins: Structure Function, and Genetics* 8: 195-202 (1990).
	✓	Gribskov, M. and R.R. Burgess., Sigma factors from *E. coli, B. subtilis,* phage SP01, and phage T4 are homologous proteins, *Nucl. Acids Res.* 14(1): 6745-63 (1986).
not considered		~~*Guide to Human Genome Computing* Bishop, M., ed. Academic Press, Inc., San Diego~~ (1994). No copy provided
	✓	Gulnik *et al.* Kinetic Characterization and Cross-Resistance Patterns of HIV-1 Protease Mutants Selected under Drug Pressure, *Biochemistry* 35: 9282-7 (1995).
	✓	Habuka *et al.* Crystal Structure of HCV NS3 protease, *Jikken Igaku* 15(19): ~~2308-13~~ (1997). no translation or statement of relevance
	✓	Hess *et al.*, Impact of Pharmacogenomics on the Clinical Laboratory, Molecular Diagnosis 4(4):289-98 (1999).
	✓	Higgins *et al.*, CABIOS, 8:189-191 (1991)
*		Ingallinella *et al.*, Potent Peptide Inhibitors of Human Hepatitis C Virus NS3 Protease Are Obtained by Optimizing the Cleavage Products, Biochemistry. 37:8906-8914 (1998).
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